

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:44:30 ; Search time 816 Seconds
(without alignments)
780.321 Million cell updates/sec

Title: US-10-604-944A-14
Perfect score: 77
Sequence: 1 ttaccctatagtcgagaaca.....aactttaaatgcatgggttaa 77

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	77	8	US-10-604-944-14
2	77	100.0	845	3	US-09-756-551A-3
3	77	100.0	1092	5	US-10-003-035-34
4	77	100.0	1092	6	US-10-286-332A-34
5	77	100.0	1092	6	US-10-280-915-34
6	77	100.0	1092	8	US-10-286-332A-34
7	77	100.0	1092	8	US-10-280-915-34
8	77	100.0	1179	5	US-10-003-035-35
9	77	100.0	1179	6	US-10-286-332A-35
10	77	100.0	1179	6	US-10-280-915-35
11	77	100.0	1179	8	US-10-286-332A-35
12	77	100.0	1179	8	US-10-280-915-35
13	77	100.0	1308	5	US-10-003-035-36
14	77	100.0	1308	6	US-10-286-332A-36
15	77	100.0	1308	6	US-10-280-915-36
16	77	100.0	1308	8	US-10-286-332A-36
17	77	100.0	1308	8	US-10-280-915-36
18	77	100.0	1496	5	US-10-003-035-17
19	77	100.0	1496	6	US-10-286-332A-17
20	77	100.0	1496	6	US-10-280-915-17
21	77	100.0	1496	8	US-10-286-332A-17
22	77	100.0	1496	8	US-10-280-915-17
23	77	100.0	1503	3	US-09-968-355-25

24	77	100.0	1503	5	US-10-097-534-31	Sequence 31, Appl
25	77	100.0	1503	6	US-10-000-511A-9	Sequence 9, Appl
26	77	100.0	1503	6	US-10-000-511A-10	Sequence 10, Appl
27	77	100.0	1503	7	US-10-384-339C-138	Sequence 138, App
28	77	100.0	1503	8	US-10-844-658-8	Sequence 8, Appl
29	77	100.0	1515	6	US-10-102-622-5	Sequence 5, Appl
30	77	100.0	1548	3	US-09-968-355-19	Sequence 19, Appl
31	77	100.0	1596	3	US-09-968-355-22	Sequence 22, Appl
32	77	100.0	1621	3	US-09-882-945A-158	Sequence 158, App
33	77	100.0	1621	8	US-10-807-114-158	Sequence 158, App
34	77	100.0	1752	3	US-09-968-355-16	Sequence 16, Appl
35	77	100.0	1800	5	US-10-003-035-58	Sequence 58, Appl
36	77	100.0	1800	6	US-10-286-332A-58	Sequence 58, Appl
37	77	100.0	1800	6	US-10-280-915-58	Sequence 58, Appl
38	77	100.0	1800	8	US-10-286-332A-58	Sequence 58, Appl
39	77	100.0	1800	8	US-10-280-915-58	Sequence 58, Appl
40	77	100.0	2460	8	US-10-483-654-30	Sequence 30, Appl
41	77	100.0	3477	6	US-10-336-566-87	Sequence 87, Appl
42	77	100.0	3479	7	US-10-646-628-5	Sequence 5, Appl
43	77	100.0	3807	6	US-10-441-788-78	Sequence 78, Appl
44	77	100.0	4307	3	US-09-999-183-1	Sequence 1, Appl
45	77	100.0	4307	6	US-10-351-938-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-604-944-14
; Sequence 14, Application US/10604944
; Publication No. US20040219515A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALY DETECTABLE GROUP OF NOVEL HIV REGULATORY GENES
; FILE REFERENCE: 55008
; CURRENT APPLICATION NUMBER: US/10/604,944
; CURRENT FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14:
; LENGTH: 77
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus 1
US-10-604-944-14

Query Match 100.0%; Score 77; DB 8; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.7e-18;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TTACCCTATAGTCGAGAACATCCAGGGGCAATGTCATCATCAGGCCATATCACCTAGAAC	60
DB	1	TTACCCTATAGTCGAGAACATCCAGGGGCAATGTCATCATCAGGCCATATCACCTAGAAC	60
QY	61	TTTAAATGCAATGGGTAA	77
DB	61	TTTAAATGCAATGGGTAA	77

RESULT 2
US-09-756-551A-3
; Sequence 3, Application US/09756551A
; Patent No. US20020051768A1
; GENERAL INFORMATION:
; APPLICANT: C. Morrow et al.
; TITLE OF INVENTION: ENCAPSATED RECOMBINANT VIRAL
; TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 STATE STREET
; CITY: BOSTON

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:52:42 ; Search time 405 Seconds
(without alignments)
157.929 Million cell updates/sec

Title: US-10-604-944A-14
Perfect score: 77
Sequence: 1 ttaccttagtgagaaca.....aactttaaatgcatggtaa 77

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6059551 seqs, 41533918 residues

Total number of hits satisfying chosen parameters: 12119102

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New.*

- 1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	1515	7	US-10-507-928-5
2	77	100.0	1515	8	US-11-029-465-5
3	77	100.0	9719	10	US-11-042-988-10
4	75.4	97.9	1503	7	US-10-519-531-2
5	75.4	97.9	16360	7	US-10-519-531-1
6	75.4	97.9	17207	7	US-10-519-531-8
7	45.6	59.2	1521	8	US-11-129-442-22
8	44	57.1	1503	7	US-10-507-928-3
9	44	57.1	1503	8	US-11-029-465-3
10	44	57.1	1518	8	US-10-507-928-7
11	44	57.1	1518	8	US-11-029-465-7
12	42.4	55.1	1092	8	US-11-014-842A-40
13	42.4	55.1	5278	8	US-11-124-602-2
14	42.4	55.1	5304	8	US-11-124-602-1
15	28.2	36.6	1329	7	US-10-750-185-37952
16	28.2	36.6	1329	7	US-10-750-185-37952
17	26.4	34.3	1691140	8	US-11-091-018-1
18	25.8	33.5	697	7	US-10-750-185-28849
19	25.8	33.5	697	7	US-10-750-185-28849
20	24.8	32.2	98345	8	US-11-112-908-36
21	24.8	32.2	127340	8	US-11-112-908-35
22	24.4	31.7	1086	7	US-10-750-185-32559

C 23	24.4	31.7	1086	7	US-10-750-623-32559	Sequence 32559, A
C 24	24.2	31.4	28033	7	US-10-829-826B-42	Sequence 42, Appl
C 25	24.2	31.4	28033	7	US-10-829-826B-43	Sequence 43, Appl
C 26	23.8	30.9	643	8	US-11-043-752-1480	Sequence 1480, Ap
C 27	23.8	30.9	1280	7	US-10-750-185-53636	Sequence 53636, A
C 28	23.8	30.9	1280	7	US-10-750-623-53636	Sequence 53636, A
C 29	23.8	30.9	387780	7	US-10-995-561-13259	Sequence 13259, A
C 30	23.6	30.6	480	8	US-11-219-146-33	Sequence 33, Appl
C 31	23.6	30.6	480	8	US-11-219-146-35	Sequence 35, Appl
C 32	23.6	30.6	480	8	US-11-219-146-37	Sequence 37, Appl
C 33	23.6	30.6	480	8	US-11-219-146-39	Sequence 39, Appl
C 34	23.6	30.6	600	8	US-11-219-146-41	Sequence 41, Appl
C 35	23.6	30.6	600	8	US-11-219-146-43	Sequence 43, Appl
C 36	23.6	30.6	600	8	US-11-219-146-45	Sequence 45, Appl
C 37	23.6	30.6	600	8	US-11-219-146-47	Sequence 47, Appl
C 38	23.6	30.6	752	8	US-11-219-146-17	Sequence 17, Appl
C 39	23.6	30.6	752	8	US-11-219-146-19	Sequence 19, Appl
C 40	23.6	30.6	752	8	US-11-219-146-21	Sequence 21, Appl
C 41	23.6	30.6	752	8	US-11-219-146-23	Sequence 23, Appl
C 42	23.6	30.6	1151	8	US-11-219-146-1	Sequence 1, Appl
C 43	23.6	30.6	1151	8	US-11-219-146-3	Sequence 3, Appl
C 44	23.6	30.6	1151	8	US-11-219-146-5	Sequence 5, Appl
C 45	23.6	30.6	1151	8	US-11-219-146-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-10-507-928-5
; Sequence 5, Application US/10507928
; Publication No. US20050266024A1
; GENERAL INFORMATION:
; APPLICANT: POWDERED LIMITED AND GLAXO GROUP LIMITED
; TITLE OF INVENTION: ADJUVANT
; FILE REFERENCE: N.88232B GCW
; CURRENT APPLICATION NUMBER: US/10/507,928
; CURRENT FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence of the p17/24trNEF insert in p17/24trNEF1
US-10-507-928-5

Query Match 100.0%; Score 77; DB 7; Length 1515;
Best Local Similarity 100.0%; Pred. No. 4.3e-20;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TTACCTTATAGTGCAGAACATCCAGGGCAATGTACATCAGGCCATATCACCTAGAAC	60
Db	393	TTACCTTATAGTGCAGAACATCCAGGGCAATGTACATCAGGCCATATCACCTAGAAC	452
Qy	61	TTTAAATGCATGGGTAA	77
Db	453	TTTAAATGCATGGGTAA	469

RESULT 2
US-11-029-465-5
; Sequence 5, Application US/11029465
; Publication No. US20050256070A1
; GENERAL INFORMATION:
; APPLICANT: Thomsen, Ralph P.
; APPLICANT: Braun, Ralph P.
; APPLICANT: Thomsen, Lindy
; APPLICANT: Van-Wely, Catherine
; APPLICANT: Ertl, Peter
; TITLE OF INVENTION: Adjuvant
; FILE REFERENCE: 033267-015
; CURRENT APPLICATION NUMBER: US/11/029,465

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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 10:41:26 ; Search time 142 Seconds
(without alignments)
963.889 Million cell updates/sec

Title: US-10-604-944A-14

Perfect score: 77

Sequence: 1 ttacctatagtcgaaca.....aactttaatgcgtggttaa 77

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/6C COMB.seq.*
6: /cgn2_6/ptodata/1/ina/6D COMB.seq.*
7: /cgn2_6/ptodata/1/ina/6E COMB.seq.*
8: /cgn2_6/ptodata/1/ina/6F COMB.seq.*
9: /cgn2_6/ptodata/1/ina/6G COMB.seq.*
10: /cgn2_6/ptodata/1/ina/6H COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	840	2	US-07-979-966A-1
2	77	100.0	845	2	US-08-589-446-3
3	77	100.0	845	2	US-08-444-882-3
4	77	100.0	845	2	US-08-389-459A-3
5	77	100.0	845	3	US-08-987-867A-3
6	77	100.0	1314	3	US-08-392-794A-1
7	77	100.0	2095	2	US-08-333-901-5
8	77	100.0	2095	2	US-08-456-582-5
9	77	100.0	2095	2	US-08-898-789-5
10	77	100.0	3807	2	US-08-417-210A-78
11	77	100.0	3807	3	US-09-136-159A-78
12	77	100.0	4307	3	US-09-552-950-1
13	77	100.0	4307	3	US-09-936-572-1
14	77	100.0	4338	3	US-09-872-733A-1
15	77	100.0	5362	3	US-08-463-210-5
16	77	100.0	5362	3	US-08-463-028-5
17	77	100.0	5362	3	US-08-463-209-5
18	77	100.0	7228	2	US-08-850-049-128
19	77	100.0	7228	2	US-08-850-049-129
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21	77	100.0	7228	2	US-08-050-478-129
22	77	100.0	7228	3	US-09-414-117-128
23	77	100.0	7228	3	US-09-414-117-129
24	77	100.0	7228	3	US-09-678-437-128

25	77	100.0	7228	3	US-09-678-437-129	Sequence 129, App
26	77	100.0	7228	3	US-09-943-722-128	Sequence 128, App
27	77	100.0	7228	3	US-09-943-722-129	Sequence 129, App
28	77	100.0	8366	3	US-09-872-733A-6	Sequence 129, Appli
29	77	100.0	8560	3	US-09-936-572-11	Sequence 11, Appli
30	77	100.0	8932	3	US-09-124-900-1	Sequence 1, Appli
31	77	100.0	8933	3	US-08-463-210-4	Sequence 4, Appli
32	77	100.0	8933	3	US-09-620-958A-3	Sequence 3, Appli
33	77	100.0	8933	3	US-09-620-958A-9	Sequence 4, Appli
34	77	100.0	8933	3	US-08-463-028-4	Sequence 9, Appli
35	77	100.0	8933	3	US-08-463-028-4	Sequence 4, Appli
36	77	100.0	8933	3	US-09-943-286-3	Sequence 3, Appli
37	77	100.0	8933	3	US-09-943-286-3	Sequence 4, Appli
38	77	100.0	8933	3	US-09-943-286-4	Sequence 3, Appli
39	77	100.0	8933	3	US-09-943-286-4	Sequence 4, Appli
40	77	100.0	9609	3	US-09-943-286-9	Sequence 3, Appli
41	77	100.0	9719	3	US-09-700-304-1	Sequence 4, Appli
42	75.4	97.9	1503	3	US-09-393-795-2	Sequence 1, Appli
43	75.4	97.9	7399	2	US-08-418-848A-9	Sequence 9, Appli
44	75.4	97.9	9709	2	US-08-188-583-5	Sequence 5, Appli
45	75.4	97.9	9709	3	US-08-388-353-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-07-979-966A-1
; Sequence 1, Application US/07979966A
; Patent No. 5707864
; GENERAL INFORMATION:
; APPLICANT: Myron E. Essex
; APPLICANT: Xiaofang Yu
; APPLICANT: Tun-Hou Lee
; TITLE OF INVENTION: AIDS THERAPEUTICS BASED ON HIV
; TITLE OF INVENTION: MA PEPTIDES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/979,966A
; FILING DATE: No. 5707864ember 23, 1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00379/018001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 840
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-979-966A-1

Query Match 100.0%; Score 77; DB 2; Length 840;